

SEQUENCE LISTING

<110> Reed, Guy L.

<120> Composition and Method for Enhancing Fibrinolysis

<130> 0609.4320003

<140>

<141> 2001-10-12

<150> 08/934,000

<151> 1997-09-19

<150> 60/026,356

<151> 1996-09-20

<160> 81

<170> PatentIn version 3.1

<210> 1

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<213> Artificial Sequence

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<223> Alpha-2 Antiplasmin Antibody

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<222> (1)..(1)  
<223> May be any Amino Acid

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Xaa Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val  
1 5 10 15

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Asp Ile Gln Met Thr  
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<220>

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<222> (1)..(381)

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<222> (1)..(60)

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Met Ser Val Leu Thr Gln Val Leu Xaa Leu Leu Leu Trp Leu Thr  
-20 -15 -10 -5

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96  
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
1 5 10

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat 144  
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn  
15 20 25

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct 192  
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
30 35 40

cag ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca 240

Gln	Leu	Leu	Val	Tyr	Asn	Ala	Lys	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser
45									55						60
agg	ttc	agt	ggc	agt	gga	tca	gga	aca	caa	ttt	tct	ctc	agg	atc	aac
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ser	Leu	Arg	Ile	Asn
									65					75	
agc	ctg	cag	cct	gaa	gat	ttt	ggg	agt	cat	tac	tgt	caa	cat	ttt	tgg
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Gly	Ser	His	Tyr	Cys	Gln	His	Phe	Trp
									80					90	
acc	act	ccg	tgg	acg	ttc	ggt	gga	ggc	acc	aag	ctg	gaa	atc	aaa	
Thr	Thr	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
									95					105	

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<222> (9) .. (9)

<223> May be either Gly or Ala

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Gly	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser
						1			5				10		

Ala	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gly	Asn
						15		20					25		

Ile	His	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro
								30	35				40		

Gln	Leu	Leu	Val	Tyr	Asn	Ala	Lys	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser
45									50					55	60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn  
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp  
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
95 100 105

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<222> (1)..(60)

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atg agt gtg ctc act cag gtc ctg ggg ttg ctg ctg tgg ctt aca  
Met Ser Val Leu Thr Gln Val Leu Gly Leu Leu Leu Trp Leu Thr  
-20 -15 -10 -5

48

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct  
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
1 5 10

96

gca tct gtg gga gaa act gtc acc gtc aca tgt cga gca agt ggg aat  
Ala Ser Val Gly Glu Thr Val Thr Cys Arg Ala Ser Gly Asn

144

15	20	25	
att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro	30	35	40
cag ctc ctg gtc tat aat gca aga acc tta gca gat ggt gtg cca tca Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser	45	50	55
agg ttc agt ggc agt gga tca gga aca caa tat tct ctc aag atc aac Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn	65	70	75
agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp	80	85	90
agt aat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa Ser Asn Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	95	100	105

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Met Ser Val Leu Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr  
-20 -15 -10 -5

Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
1 5 10

Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn  
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
30 35 40

Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser  
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn  
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp  
80 85 90

Ser Asn Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
95 100 105

<210> 8

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-20 -15 -10 -5

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96  
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
1 5 10

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat 144  
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn  
15 20 25

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct	192
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro	
30 35 40	
caa ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca	240
Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser	
45 50 55 60	
agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc aag atc aac	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn	
65 70 75	
agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg	336
Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp	
80 85 90	
acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa	381
Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	
95 100 105	

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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
1 5 10

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn  
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser  
45 50 55 60

Arg Phe Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn

65

70

75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp  
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
95 100 105

<210> 10

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-15 -10 -5

48

ctc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag  
Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
1 5 10

96

cct gga gaa aca gtc aag atc tcc tgc aag gcc tct ggg tat acc ttc  
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25

144

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
30 35 40 45	
aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct	240
Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala	
50 55 60	
gaa gag ttc aag gga cgg ttt gtc ttc tct ttg gaa acc tct gcc agc	288
Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser	
65 70 75	
act gcc cat ttg cag atc aag aat ttc aga aat gag gac acg gct aca	336
Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr	
80 85 90	
tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg	384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp	
95 100 105	
ggt caa gga acc tca gtc acc gtc tcc tca	414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
110 115	
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<223> May be either Asp or Ala	
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Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser

-15

-10

-5

Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu  
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala  
50 55 60

Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser  
65 70 75

Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr  
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp  
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
110 115

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-15                  -10                  -5		
atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag		96
Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys		
1                  5                  10		
cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc		144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
15                  20                  25		
aca aag tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta		192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu		
30                  35                  40                  45		
aag tgg atg ggc tgg ata aac acc aac agt gga gag cca aca tat gct		240
Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala		
50                  55                  60		
gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc		288
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser		
65                  70                  75		
act gcc tat ttg cag atc aac aac ctc aaa aat gag gac tcg gct aca		336
Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr		
80                  85                  90		
tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg		384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp		
95                  100                  105		
ggt caa gga acc tca gtc acc gtc tcc tca		414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser		
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<223> May be either Asp or Ala

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<223> May be either Asn or Thr

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Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser  
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Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu  
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala  
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
65 70 75

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr  
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp  
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
110 115

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-15                  -10                  -5		
atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag		96
Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys		
1                  5                  10		
cct gga gaa aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc		144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
15                  20                  25		
aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta		192
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu		
30                  35                  40                  45		
aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct		240
Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala		
50                  55                  60		
gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc		288
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser		
65                  70                  75		
act gcc aat ttg cag atc aag aac ctc aaa aat gag gac acg gct aca		336

Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr		
80	85	90
tat ttc tgt gca aga tgg gta cct ggg acc tat gcc atg gac tac tgg		384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp		
95	100	105
ggt caa gga acc tca gtc acc gtc tcc tca		414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser		
110	115	

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<223> May be either Asp or Ala

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<223> May be either Asn or Thr

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Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser		
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Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys		
1	5	10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
15	20	25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu		
30	35	40
		45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala  
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
65 70 75

Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr  
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp  
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
110 115

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Met Ser Val Leu Thr Gln Val Leu 54

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-10                    -5                    1	
act cag tct cca tcc tcc cta tct gca tct gtg gga gac aga gtc acc Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	150
5                    10                    15                    20	
atc aca tgt cga gca agt ggg aat att cac aat tat tta gca tgg tat Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala Trp Tyr	198
25                    30                    35	
cag cag aaa cag gga aaa tct cct caa ctc ctg gtc tat aat gca aaa Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys	246
40                    45                    50	
acc tta gca agt ggt gtg cca tca agg ttc agt ggc agt gga tca gga Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	294
55                    60                    65	
aca gat ttt act ctc acc atc agc agc ctg cag cct gaa gat ttt ggg Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Gly	342
70                    75                    80	
agt cat tac tgt caa cat ttt tgg acc act ccg tgg acg ttc ggt gga Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp Thr Phe Gly Gly	390
85                    90                    95                    100	
ggc acc aag ctg gaa atc aaa Gly Thr Lys Leu Glu Ile Lys	411
105	

<210> 17

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<212> PRT

<213> Artificial Sequence

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<400> 17

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Trp Leu Thr  
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
1                    5                    10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Asn  
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Ser Gly Val Pro Ser  
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp  
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
95 100 105

<210> 18

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<220>

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<222> (1)..(417)

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<222> (1)..(60)

<223>

<210> 19

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<223> Alpha-2 Antiplasmin Antibody

<400> 19

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr  
-20 -15 -10 -5

Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys  
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr  
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly  
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr  
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val  
65 70 75

Thr Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala  
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr  
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
110 115

<210> 20

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<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

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<221> CDS

<222> (31)..(447)

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Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Trp Leu Thr  
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Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys  
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr  
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly  
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr  
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr  
65 70 75

Ser Thr Ala Tyr Leu Glu Ile Arg Ser Leu Arg Ser Asp Asp Thr Ala  
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr  
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
110 115

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<223> May be any Nucleotide

<400> 22

nnnnnngaat tcactggatg gtggaaagat gga

33

<210> 23

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42

<210> 24

<211> 40

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<400> 24

actagtcgac atgagtgtgc tcactcaggt cctggsgttg

40

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tagggagacc caagcttggc accaatttaa attgatatct ccttaggtct cgagtctcta 60  
gataaccggc caatcgattt ggattctt 88

<210> 26

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gacactata gataggccccc ttccgcggtt ggatccaaca cgtgaagcta gcaagcggcc 60  
gcaagaattt caatcgattt accggta 88

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<210> 28  
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41

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32

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cttttttcc ctttttgag aggc

24

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cgcgccggct tcgaatagcc agagtaacct tttttttaa ttttatttta ttttattttt 60

gagatggagt ttgg

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attcgaagcc gg

72

<210> 33

<211> 24

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<400> 33

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<210> 34

<211> 24

<212> DNA

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<400> 34

ctcgagggt caccacgctg ctga

24

<210> 35

<211> 21

<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<400> 35

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21

<210> 36

<211> 21

<212> DNA

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<400> 36

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21

<210> 37

<211> 30

<212> DNA

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<400> 37

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30

<210> 38

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

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cttgcggccg cttgctagca tggattgggt gtggaaacttg ctattcctga tggcagctgc

60

ccaaagtatac caagcacacaga

80

<210> 39

<211> 80

<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

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60

ttggatactt tgggcagctg

80

<210> 40

<211> 80

<212> DNA

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aactatggaa tgaactgggt 80

<210> 41

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<400> 41

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tcattccata gtttgtgaag 80

<210> 42

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<400> 42

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<210> 43

<211> 80

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<400> 43  
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aaggcaaacc gtcccttgaa 80

<210> 44

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<400> 44  
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tgggacctat gccatggact 80

<210> 45

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<400> 45  
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ggcataggttc ccaggtaccc 80

<210> 46

<211> 29

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<400> 46

gggaagacgg atgggccctt ggtgcttagc

29

<210> 47

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<400> 47

attnaaatttg atatccctt aggtctcgag

30

<210> 48

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<400> 48

attnaaatttg atatccctt aggtctcgag atgagtggtc tcactcagggt cctggcggttg

60

ctgctgctgt ggcttacag

79

<210> 49

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ccacagcagc agcaacgc 78  
  
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tggaaatatt cacaatta 78  
  
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tatagaccag gagctgagga gatTTCCCT gtttctgctg ataccatgct aaataattgt 60  
gaatattccc acttgctc 78  
  
<210> 52  
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<400> 52  
aaatctcctc agtcctggc ctataatgca aaaaccttag cagatggtgt gccatcaagg 60  
ttcagtggca gtggatca 78

<210> 53

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ctccccaaaat cttcaggctg caggctgttgc atcctgagag aaaattgtgt tcctgatcca 60  
ctgccactga accttgat 78

<210> 54

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<400> 54  
gcctgcagcc tgaagatttt gggagtcatt actgtcaaca tttttggacc actccgtgga 60  
cgttcggtgg aggcacca 78

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gcctccaccg aacgtccacg g 81

<210> 56

<211> 30

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<400> 56

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<210> 57

<211> 80

<212> DNA

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<400> 57

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<210> 58

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ggcacctgtta agccacagca 80

<210> 59

<211> 80

<212> DNA

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<400> 59  
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acaaaactatg gaatgaactg 80

<210> 60

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<400> 60  
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<400> 61

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<210> 62

<211> 80

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<400> 62

ttagctttga ggctgctgat ctgcaaatacg cagtgctga cagaggtgtc caaagagaag 60  
acaaaccgttc ccttgaactc 80

<210> 63

<211> 80

<212> DNA

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<400> 63

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acctgggacc tatgccatgg 80

<210> 64

<211> 80

<212> DNA

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<400> 64

gcccttggtg ctagctgagg agacggtgac cgtggttcct tgaccccagt agtccatggc	60
ataggtccca ggtacccatc	80

<210> 65

<211> 80

<212> DNA

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<400> 65

tgcgtggct tacaggtgcc agatgtcaga tccagtttgt gcagtctgga gctgaggtga	60
agaagcctgg agcctcagtc	80

<210> 66

<211> 80

<212> DNA

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<400> 66

tagagtggat gggctggata aacaccaaga gtggagagcc aacatatgct gaagagttca	60
agggacggtt taccttcacc	80

<210> 67

<211> 80

<212> DNA

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gtaaaaccgtc ccttgaactc

80

<210> 68

<211> 80

<212> DNA

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<400> 68

tttggagatc aggaggctca gatctgacga cacggctgtg tatttctgtg caagatgggt 60

acctgggacc tatgccatgg

80

<210> 69

<211> 78

<212> DNA

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agatgcagat agggaggatg gagactgagt catctggatg tcacatctgg cacctgtaag 60

ccacagcagc agcaacgc

78

<210> 70

<211> 78

<212> DNA

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<400> 70

gtctccatcc tcccttatctg catctgtggg agacagagtc accatcacat gtcgagcaag 60  
tggaatatt cacaatta 78

<210> 71

<211> 78

<212> DNA

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<400> 71

aaatctcctc aactcctggc ctataatgca aaaaccttag caagtggtgt gccatcaagg 60  
ttcagtggca gtggatca 78

<210> 72

<211> 78

<212> DNA

<213> Artificial Sequence

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<400> 72

ctccccaaat cttcaggctg caggctgctg atggtgagag taaaatctgt tcctgatcca 60  
ctgccactga accttgat 78

<210> 73

<211> 18

<212> PRT

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<400> 73

Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu  
1 5 10 15

Thr Thr

<210> 74

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

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<400> 74

Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser  
1 5 10 15

<210> 75

<211> 107

<212> PRT

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<223> May be any Amino Acid

<400> 75

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Glu Thr Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val  
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Gln Xaa Ser Leu Xaa Ile Asn Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp  
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 76

<211> 107

<212> PRT

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<222> (74) .. (74)

<223> May be any Amino Acid

<400> 76

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val  
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Xaa Ile Asn Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp  
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 77

<211> 107

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<400> 77

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1 5 10 15

Xaa Xaa Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val  
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Xaa Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Xaa Xaa Xaa Leu Xaa Ile Xaa Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp  
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 78

<211> 119

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<400> 78

Gln Ile Gln Leu Val Gln Ser Gly Xaa Glu Xaa Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe  
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Asp Thr Ser Xaa Ser Thr Ala Tyr  
65 70 75 80

Leu Xaa Ile Xaa Ser Leu Xaa Xaa Xaa Asp Thr Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Thr Val Thr Val Ser Ser  
115

<210> 79

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<212> PRT

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<400> 79

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15

Thr Val Lys Ile Ser Cys Xaa Ala Ser Gly Tyr Thr Phe Thr Xaa Tyr  
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe  
50 55 60

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa  
65 70 75 80

Leu Gln Ile Xaa Asn Xaa Xaa Asn Glu Asp Xaa Ala Thr Tyr Phe Cys  
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Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
35 40 45

Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe  
50 55 60

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa  
65 70 75 80

Leu Gln Ile Lys Asn Xaa Xaa Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
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20 25 30

Gly Met Asn Trp Val Xaa Gln Ala Pro Gly Xaa Gly Leu Xaa Trp Met  
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe  
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Xaa Thr Ser Xaa Ser Thr Ala Xaa  
65 70 75 80

Leu Xaa Ile Xaa Xaa Xaa Xaa Xaa Asp Xaa Ala Xaa Tyr Phe Cys  
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Xaa Val Thr Val Ser Ser  
115